

7,9000



SEQUENCE LISTING

#3
RECEIVED
AUG 06 2001
TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

- (i) APPLICANT: Shuping Tong et al.
- (ii) TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
- (iii) NUMBER OF SEQUENCES: 75
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C.
 - (B) STREET: 225 Franklin Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/683,262
 - (B) FILING DATE: 18-JUL-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Clark, Paul T.
 - (B) REGISTRATION NUMBER: 30,162
 - (C) REFERENCE/DOCKET NUMBER: 00786/287002
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 542-5070
 - (B) TELEFAX: (617) 542-8906
 - (C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCAGATCTAT GGCAGAATC TTTCCAC

27

(2) INFORMATION FOR SEQ ID NO:2:

00018066-080201

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGAATTCAG CGCAGGGTCC CCAAT

25

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCAGATCTAT GATGGGGCAA CATCCAGC

28

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGAATTCAG GTACCAGACA TTTTCTTCTT

30

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGAATTCTT ATTCCTAACT CTTGTAA

27

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

102080-93081860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GARYTNTAYG TNATGGAGAT

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAYTCNGGYT CNCCNGCYTC RTG

23

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TKYTNAGYCA YGARTTYCAR G

21

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTKGCNGART ANARNGTYTC

20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAAACAGA CACTGAAGAA

20

(2) INFORMATION FOR SEQ ID NO:11:

090106-00001

09818065-080201

ATGGAGATCT CGGACGGCCC

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCTTCAGTG TCTGTTTCAT

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Ser Arg Arg Ala Ser Val Gly Ser
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATCACTGAGC TCAAATTACC CCATGAGATG

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAACTCGA GCTGGAAGCA GTGTTATGAA

30

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGGTACCAT GGAGGCGGCG CGGTGCATCG AGC

33

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCTCGAGAT ATTAACATTA GCAATGTTAC T

31

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gln	Trp	Thr	Pro	Glu	Glu	Asp	Gln	Lys	Ala	Arg	Glu	Ala	Phe	Arg	Arg
1				5				10					15		

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

T02030" 33031350

0981806E 080207

Gly Val His Glu Ala Gly Glu Pro Glu Phe Lys
20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

Leu Ile Asp Arg Thr Arg Ile Val Ile Val Pro Ser Leu Asn Pro Asp
1 5 10 15

Gly Arg Ile Ala
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

Ser Leu Leu Ser His Glu Phe Gln Asp Glu Thr Asp Thr Glu Glu Glu
1 5 10 15

Thr Leu Tyr Ser Ala Lys
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

Val Glu Glu Gly Lys Val Pro Val Leu Asn Thr Pro Asp
1 5 10

SECRET

(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

Glu Leu Tyr Val Met Glu Ile Ser Asp Asn Pro Gly Val His Glu Ala
1 5 10 15
Gly Glu Pro Glu Phe Lys
20

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "X is A or G."
```

GAXCTNTAYG TNATGGAXAT WAGYGAYAAY CCNGGNGTNC AYGAXGCNGG NGAXCCNGAX	60
TTYAAX	66

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "X is A or G."

GAXTTXTAYG TNATGGAXAT WTCNGAYAAY CCNGGNGTNC AYGAXGCNGG NGAXCCNGAX	60
TTYAAX	66

090100Z 080201

(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "X is A or G."

GAXYTNTAYG TNATGGAGAT CTCGGACAAC CCCGGYGYTC AYGAXGCNGG NGAXCCNGAX	60
TT	62

(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

ATGGAGATCT CGGACAACCC CGGCGTCCAT GAAGCAGGTG AGCCAGAGTT CAAG 54

(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

Ser Leu Leu Ser His Glu Phe Gln Asp Glu Thr Asp Thr Glu Glu Glu
1 5 10 15
Thr Leu Tyr Ser Ala Lys
20

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(D) OTHER INFORMATION: /note= "X at positions 18, 24, 30, 42, 45, 48, and 66 is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGYCTNCTNA GYCAYGAXTT YCAXGAYGAX ACNGAYACNG AXGAXGAXAC NCTNTAYAGY 60

GCNAAX 66

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(D) OTHER INFORMATION: /note= "X at positions 6, 9, 18, 24, 30, 42, 45, 48, 54, and 66 is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TCNTTXXTTXT CNCAYGAXTT YCAXGAYGAX ACNGAYACNG AXGAXGAXAC NTTXTAYTCN 60

GCNAAX 66

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(D) OTHER INFORMATION: /note= "Z at position 2 is G or T, X at positions 14, 20, and 44 is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TZYTNAAGYCA YGAXTTYCAX GATGAAACAG AACTGAAGA AGAXACNYTN TAYTCNGCVA 60

A 61

TOEBOE "9903T360

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCCCTTTTGA GCCACGAATT CCAGGATGAA ACAGACACTG AAGAA

45

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATG GGG CAA CAT CCA GCA AAA TCA ATG GAC GTC AGA CGG ATA GAA GGA	48
Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly	
1 5 10 15	
GGA GAA ATA CTG TTA AAC CAA CTT GCC GGA AGG ATG ATC CCA AAA GGG	96
Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly	
20 25 30	
ACT TTG ACA TGG TCA GGC AAG TTT CCA ACA CTA GAT CAC GTG TTA GAC	144
Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp	
35 40 45	
CAT GTG CAA ACA ATG GAG GAG ATA AAC ACC CTC CAG AAT CAG GGA GCT	192
His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala	
50 55 60	
TGG CCT GCT GGG GCG GGA AGG AGA GTA GGA TTA TCA AAT CCG ACT CCT	240
Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro	
65 70 75 80	
CAA GAG ATT CCT CAG CCC CAG TGG ACT CCC GAG GAA GAC CAA AAA GCA	288
Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala	
85 90 95	
CGC GAA GCT TTT CGC CGT TAT CAA GAA GAA AGA CCA CCG GAA ACC ACC	336
Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr	
100 105 110	

102030-93031360

ACC ATT CCT CCG TCT TCC CCT CCT CAG TGG AAG CTA CAA CCC GGG GAC	384
Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp	
115 120 125	
GAT CCA CTC CTG GGA AAT CAG TCT CTC CTC GAG ACT CAT CCG CTA TAC	432
Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr	
130 135 140	
CAG TCA GAA CCA GCG GTG CCA GTG ATA AAA ACT CCC CCC TTG AAG AAG	481
Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys	
145 150 155 160	
AAA	483
Lys	

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly	
1 5 10 15	
Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly	
20 25 30	
Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp	
35 40 45	
His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala	
50 55 60	
Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro	
65 70 75 80	
Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala	
85 90 95	
Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr	
100 105 110	
Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp	
115 120 125	
Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr	
130 135 140	

102020-99021350

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Lys	Gly	Met	Gly	Thr	Asn	Leu	1	5	10	15
Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Leu	Pro	Asp	His	Gln	Leu	Asp	Pro	20	25	30	
Ala	Phe	Gly	Ala	Asn	Ser	Thr	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Ile	35	40	45	
Lys	Asp	His	Trp	Pro	Ala	Ala	Asn	Gln	Val	Gly	Val	Gly	Ala	Phe	Gly	50	55	60	
Pro	Gly	Leu	Thr	Pro	Pro	His	Gly	Gly	Ile	Leu	Gly	Trp	Ser	Pro	Gln	65	70	75	80
Ala	Gln	Gly	Ile	Leu	Thr	Thr	Val	Ser	Thr	Ile	Pro	Pro	Pro	Ala	Ser	85	90	95	
Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro	Pro	Leu	100	105	110	
Arg	Asp	Ser	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Ala	Leu	His	115	120	125	
Gln	Ala	Leu	Gln	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Leu	Pro	Ala	Gly	130	135	140	
Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Ala	Pro	Asn	Ile	Ala	Ser	His	145	150	155	160
Ile	Ser	Ser	Ile	Ser	Ala	Arg	Thr	Gly	Asp	Pro	Val	Thr	Ile			165	170		

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu

10202020-9903T860

102030-39081360

50		55		60
Pro Gly Phe Thr Pro	Pro His Gly Gly Leu	Leu Gly Trp Ser Pro	Gln	
65	70	75	80	
Ala Gln Gly Ile Leu	Thr Thr Val Pro	Thr Ala Pro Pro	Pro Ala Ser	
	85	90	95	
Thr Asn Arg Gln Leu	Gly Arg Lys Pro	Thr Pro Leu Ser	Pro Pro Leu	
	100	105	110	
Arg Asp Thr His Pro	Gln Ala Met Gln	Trp Asn Ser Thr	Thr Phe His	
	115	120	125	
Gln Thr Leu Gln Asp	Pro Arg Val Arg	Ala Leu Tyr Phe	Pro Ala Gly	
	130	135	140	
Gly Ser Ser Ser Gly	Thr Val Asn Pro	Val Gln Asn Thr	Val Ser Ser	
	145	150	155	160
Ile Ser Ser Ile Leu	Ser Lys Thr Gly	Asp Pro Val Pro	Asn	
	165	170		

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Gly Gly Trp Ser	Ser Lys Pro Arg	Gln Gly Met Gly	Thr Asn Leu	
1	5	10	15	
Ser Val Pro Asn Pro	Leu Gly Phe Phe	Pro Asp His Gln	Leu Asp Pro	
	20	25	30	
Ala Phe Lys Ala Asn	Ser Asp Asn Pro	Asp Trp Asp Leu	Asn Pro His	
	35	40	45	
Lys Asp Asn Trp Pro	Asp Ser Asn Lys	Val Gly Val Gly	Ala Phe Gly	
	50	55	60	
Pro Gly Phe Thr Pro	Pro His Gly Gly	Leu Leu Gly Trp	Ser Pro Gln	
	65	70	75	80
Ala Gln Gly Ile Leu	Thr Thr Val Pro	Thr Ala Pro Pro	Pro Ala Ser	
	85	90	95	
Thr Asn Arg Gln Leu	Gly Arg Lys Pro	Thr Pro Leu Ser	Pro Pro Leu	

100

105

110

Arg Asp Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
115 120 125

Gln Thr Leu Gln Asp Pro Arg Val Arg Ala Leu Tyr Phe Pro Ala Gly
130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Gln Asn Thr Ala Ser Ser
145 150 155 160

Ile Ser Ser Ile Leu Ser Thr Thr Gly Asp Pro Val Pro Asn
165 170

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Lys Ala Asn Ser Glu Asn Pro Asp Trp Asp Leu Asn Pro Asn
35 40 45

Lys Asp Asn Trp Pro Asp Ala Asn Lys Val Gly Val Gly Ala Phe Gly
50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
65 70 75 80

Ala Gln Gly Leu Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser
85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu
100 105 110

Arg Asp Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
115 120 125

Gln Thr Leu Gln Asp Pro Gly Val Arg Ala Leu Tyr Phe Pro Ala Gly
130 135 140

Gly Ser Ser Ser Gly Thr Val Ser Pro Ala Gln Asn Thr Val Ser Ala

102080-9908T860

145 150 155 160

Ile Ser Ser Ile Leu Ser Lys Thr Gly Asp Pro Val Pro Asn

165 170

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Lys	Gly	Met	Gly	Thr	Asn	Leu	1	5	10	15
Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro	20	25	30	
Ala	Phe	Lys	Ala	Asn	Ser	Glu	Asn	Pro	Asp	Trp	Asp	Leu	Asn	Pro	His	35	40	45	
Lys	Asp	Asn	Trp	Pro	Asp	Ala	His	Lys	Val	Gly	Val	Gly	Ala	Phe	Gly	50	55	60	
Pro	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser	Pro	Gln	65	70	75	80
Ala	Gln	Gly	Ile	Leu	Ser	Ser	Val	Pro	Ala	Ala	Pro	Pro	Pro	Ala	Ser	85	90	95	
Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Ile	Pro	Leu	Ser	Pro	Pro	Leu	100	105	110	
Arg	Asp	Thr	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr	Phe	His	115	120	125	
Gln	Thr	Leu	Gln	Asp	Pro	Arg	Val	Arg	Ala	Leu	Tyr	Phe	Pro	Ala	Gly	130	135	140	
Gly	Ser	Ser	Ser	Gly	Thr	Val	Ser	Pro	Ala	Gln	Asn	Thr	Val	Ser	Ala	145	150	155	160
Ile	Ser	Ser	Ile	Leu	Ser	Lys	Thr	Gly	Asp	Pro	Val	Pro	Asn			165	170		

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 174 amino acids

102030" 99081360

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Gln	Gly	Met	Gly	Thr	Asn	Leu	1	5	10	15
Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro	20	25	30	
Ala	Phe	Gly	Ala	Asn	Ser	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Asn	35	40	45	
Lys	Asp	His	Trp	Pro	Glu	Ala	Asn	Gln	Val	Gly	Ala	Gly	Ala	Phe	Gly	50	55	60	
Pro	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser	Pro	Gln	65	70	75	80
Ala	Gln	Gly	Ile	Leu	Thr	Thr	Val	Pro	Ala	Ala	Pro	Pro	Pro	Ala	Ser	85	90	95	
Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro	Pro	Leu	100	105	110	
Arg	Asp	Ser	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr	Phe	His	115	120	125	
Gln	Ala	Leu	Leu	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro	Ala	Gly	130	135	140	
Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Val	Pro	Thr	Thr	Ala	Ser	Pro	145	150	155	160
Ile	Ser	Ser	Thr	Glu	Ser	Arg	Thr	Gly	Asp	Pro	Ala	Pro	Asn			165	170		

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu

102080-93021260

102030-99081860

1		5		10		15									
Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro
		20						25					30		
Ala	Phe	Gly	Ala	Asn	Ser	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Asn
		35					40					45			
Lys	Asp	His	Trp	Pro	Glu	Ala	Asn	Gln	Val	Gly	Ala	Gly	Ala	Phe	Gly
	50						55				60				
Pro	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser	Pro	Gln
65					70					75					80
Ala	Gln	Gly	Ile	Leu	Thr	Thr	Val	Pro	Ala	Ala	Pro	Pro	Pro	Ala	Ser
			85						90					95	
Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro	Pro	Leu
		100						105					110		
Arg	Asp	Ser	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr	Phe	His
		115					120					125			
Gln	Ala	Leu	Leu	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro	Ala	Gly
	130					135					140				
Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Val	Pro	Thr	Thr	Ala	Ser	Pro
145					150					155					160
Ile	Ser	Ser	Ile	Ser	Phe	Ser	Thr	Gly	Asp	Pro	Ala	Pro	Asn		
			165						170						

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Gln	Gly	Met	Gly	Thr	Asn	Leu
1				5					10					15	
Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro
		20						25					30		
Ala	Phe	Gly	Ala	Asn	Ser	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Asn
		35					40					45			
Lys	Asp	His	Trp	Pro	Glu	Ala	Ile	Lys	Val	Gly	Ala	Gly	Asp	Phe	Gly

60

Ile Ser Ser Ile Ser Phe Ser Thr Gly Asp Pro Ala Pro Asn
165 170

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEOUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu

THE UNIVERSITY OF CHICAGO

102080"9308T850

100	105	110
Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His		
115	120	125
Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly		
130	135	140
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro		
145	150	155
Ile Ser Ser Ile Ser Ser Arg Thr Gly Asp Pro Ala Pro Asn		
165	170	

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu		
1	5	10
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro		
20	25	30
Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn		
35	40	45
Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly		
50	55	60
Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln		
65	70	75
Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser		
85	90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu		
100	105	110
Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His		
115	120	125
Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly		
130	135	140
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro		

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Gln	Gly	Met	Gly	Thr	Asn	Leu	1	5	10	15
Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro	20	25	30	
Ala	Phe	Gly	Ala	Asn	Ser	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Asn	35	40	45	
Lys	Asp	His	Trp	Pro	Glu	Ala	Asn	Gln	Val	Gly	Ala	Gly	Ala	Phe	Gly	50	55	60	
Pro	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser	Pro	Gln	65	70	75	80
Ala	Gln	Gly	Ile	Leu	Thr	Thr	Val	Pro	Val	Ala	Pro	Pro	Pro	Ala	Ser	85	90	95	
Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro	Pro	Leu	100	105	110	
Arg	Asp	Ser	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr	Phe	His	115	120	125	
Gln	Ala	Leu	Leu	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro	Ala	Gly	130	135	140	
Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Val	Pro	Thr	Thr	Ala	Ser	Pro	145	150	155	160
Ile	Ser	Ser	Ile	Phe	Ser	Arg	Thr	Gly	Asp	Pro	Ala	Pro	Asn	165	170				

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu

102030-99021250

102030-99081260

50	55	60
Pro Gly Phe Thr Pro Pro His Gly Leu Ile Leu Gly Trp Ser Pro Gln		
65	70	75 80
Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Ser Ala Ser		
	85	90 95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu		
	100	105 110
Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe Gln		
	115	120 125
Gln Ala Leu Gln Asp Pro Arg Val Arg Val Leu Tyr Phe Pro Ala Gly		
	130	135 140
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Leu		
	145	150 155 160
Ile Ser Ser Ile Phe Ser Arg Ile Gly Asp Pro Val Thr Asn		
	165	170

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu		
1	5	10 15
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro		
	20	25 30
Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn		
	35	40 45
Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly		
	50	55 60
Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln		
	65	70 75 80
Ala Gln Gly Ile Leu Thr Thr Leu Pro Ala Ala Pro Pro Pro Ala Ser		
	85	90 95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu		

100

105

110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe Gln
115 120 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Leu
145 150 155 160

Ile Ser Ser Ile Ser Phe Ser Thr Gly Asp Pro Val Thr Asn
165 170

(2) INFORMATION FOR SEO ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Gln Asn Leu
1 5 10 15

Ser Thr Ser Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Arg Ala Asn Thr Ala Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp Thr Trp Pro Asp Ala Asn Lys Val Gly Ala Gly Ala Phe Gly
50 55 60

Leu Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
65 70 75 80

Ala Gln Gly Ile Leu Glu Leu Pro Ala Asn Ile Pro Pro Pro Ala Ser
85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu
100 105 110

Arg Asn Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Ala Phe His
115 120 125

Gln Thr Leu Gln Asp Pro Arg Val Arg Gly Leu Tyr Leu Pro Ala Gly
130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Ala Pro Asn Ile Ala Ser His

09718056-080201

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gln Thr Asn Leu
1           5           10           15

Thr Ser Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20           25           30

Ala Phe Arg Ala Asn Thr Ala Asn Pro Asp Trp Asp Phe Asn Pro Asn
35           40           45

Lys Asp Ser Trp Pro Asp Ala Asn Lys Val Gly Ala Gly Ala Phe Gly
50           55           60

Leu Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
65           70           75           80

Ala Gln Gly Ile Leu Gln Thr Leu Pro Ala Asn Pro Pro Pro Ala Ser
85           90           95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu
100          105          110

Arg Asn Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
115          120          125

Gln Thr Leu Gln Asp Pro Arg Val Arg Gly Leu Tyr Leu Pro Ala Gly
130          135          140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro
145          150          155          160

Ile Ser Ser Ile Phe Ser Arg Thr Ile Asp Pro Ala Leu Asn
165          170

```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Gln Asn Leu

```

102030-59031860

102080-99081860

1	5	10	15
Ser Thr Ser Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro	20	25	30
Ala Phe Arg Ala Asn Thr Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn	35	40	45
Lys Asp Thr Trp Pro Asp Ala Asn Lys Val Gly Ala Gly Ala Phe Gly	50	55	60
Leu Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln	65	70	75
Ala Gln Gly Ile Ile Gln Thr Leu Pro Ala Asn Pro Pro Pro Ala Ser	85	90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu	100	105	110
Arg Thr Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His	115	120	125
Gln Thr Leu Gln Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly	130	135	140
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro	145	150	155
Ile Ser Ser Ile Phe Ser Arg Ile Gly Asp Pro Ala Leu Asn	165	170	

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Gln Asn Leu	1	5	10	15
Ser Thr Ser Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro	20	25	30	
Ala Phe Arg Ala Asn Thr Ala Asn Pro Asp Trp Asp Phe Asn Pro Asn	35	40	45	
Lys Asp Thr Trp Pro Asp Ala Asn Lys Val Gly Ala Gly Ala Phe Gly				

50					55					60					
Leu 65	Gly	Phe	Thr	Pro	Pro 70	His	Gly	Gly	Leu	Leu 75	Gly	Trp	Ser	Pro	Gln 80
Ala	Gln	Gly	Ile	Leu 85	Gln	Thr	Val	Pro	Ala 90	Asn	Pro	Pro	Pro	Ala 95	Ser
Thr	Asn	Arg	Gln 100	Ser	Gly	Arg	Gln	Pro 105	Thr	Pro	Leu	Ser	Pro 110	Pro	Leu
Arg	Asp	Ala 115	His	Pro	Gln	Ala	Met 120	Gln	Trp	Asn	Ser	Thr 125	Thr	Phe	His
Gln	Thr 130	Leu	Gln	Asp	Pro	Arg	Val 135	Arg	Gly	Leu	Tyr 140	Phe	Pro	Ala	Gly
Gly 145	Ser	Ser	Ser	Gly	Thr 150	Val	Asn	Pro	Val	Leu 155	Thr	Thr	Ala	Ser	Pro 160
Leu	Ser	Ser	Ile	Phe 165	Ser	Arg	Ile	Gly	Asp 170	Leu	Ala	Pro	Asn		

(2) INFORMATION FOR SEO ID NO:57:

- (A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

100

105

110

Arg Asp Ala His Pro Gln Ala Met Gln Trp Thr Ser Thr Thr Phe His
115 120 125

Gln Ala Leu Gln Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro
145 150 155 160

Ile Leu Ser Ile Phe Ser Lys Ile Gly Asp Leu Ala Pro Asn
165 170

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Gly Leu Ser Trp Thr Val Pro Leu Glu Gly Trp Gly Lys Asn His
1 5 10 15

Ser Thr Thr Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Arg Ala Asn Thr Arg Asn Pro Asp Trp Asp His Asn Pro Asn
35 40 45

Lys Asp His Trp Thr Glu Ala Asn Lys Val Gly Val Gly Ala Phe Gly
50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
65 70 75 80

Ala Gln Gly Ile Met Lys Thr Leu Pro Ala Asp Pro Pro Pro Ala Ser
85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Ile Pro Ile Thr Pro Pro Leu
100 105 110

Arg Asp Ser Thr Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
115 120 125

Gln Ala Leu Gln Asp Pro Arg Val Arg Gly Leu Tyr Leu Phe Ala Gly
130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Leu

102030" 99021250

1022030"3303T2360

1 5 10 15
Ser Val Pro Asn Pro Leu Gly Phe Leu Pro Asp His Gln Leu Asp Pro
 20 25 30
Leu Phe Arg Ala Asn Ser Ser Ser Pro Asp Trp Asp Phe Asn Thr Asn
 35 40 45
Lys Asp Ser Trp Pro Met Ala Asn Lys Val Gly Val Gly Ala Gly Tyr
 50 55 60
Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
65 70 75 80
Ala Gln Gly Val Leu Thr Thr Leu Pro Ala Asp Pro Pro Pro Ala Ser
 85 90 95
Thr Asn Arg Gln Leu Gly Arg Gln Lys Thr Gln Val Ser Pro Pro Leu
 100 105 110
Arg Asp Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr His Phe His
 115 120 125
Gln Ala Leu Leu Asp Pro Arg Val Arg Ala Leu Tyr Phe Pro Ala Gly
 130 135 140
Gly Ser Ser Ser Gly Thr Gln Asn Pro Ala Pro Thr Ile Ala Ser Leu
145 150 155 160
Thr Ser Ser Ile Ser Ser Lys Thr Gly Gly Pro Ala Met Asn
 165 170

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Gln Asn Leu
1 5 10 15
Ser Thr Ser Asn Pro Leu Gly Phe Phe Pro Glu His Gln Leu Asp Pro
 20 25 30
Ala Phe Lys Ala Asn Ser Thr Asn Pro Asp Trp Asp Phe Asn Pro Lys
 35 40 45
Lys Asp Tyr Trp Pro Glu Ala Thr Lys Val Gly Ala Gly Ala Phe Gly

102080-9908T260

50	55	60
Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Leu Ser Pro Gln		
65	70	75
80		
Ala Gln Gly Ile Leu Thr Thr Leu Pro Ala Asn Pro Pro Pro Ala Ser		
85	90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu		
100	105	110
Arg Asp Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His		
115	120	125
Gln Ala Leu Gln Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly		
130	135	140
Gly Ser Ser Ser Gly Thr Leu Asn Pro Val Pro Asn Thr Ala Ser His		
145	150	155
160		
Ile Ser Ser Val Phe Ser Thr Thr Gly Asp Pro Ala Pro Asn		
165	170	

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ATG GAG ATC TCG GAC AAC CCC GGT GTT CAT GAA GCA GGT GAG CCA GAG	48
Met Glu Ile Ser Asp Asn Pro Gly Val His Glu Ala Gly Glu Pro Glu	
165	170
175	
TTC AAG TAT ATT GGT AAC ATG CAT GGG AAT GAA GTT GTG GGG CGA GAG	96
Phe Lys Tyr Ile Gly Asn Met His Gly Asn Glu Val Val Gly Arg Glu	
180	185
190	
CTG CTC CTG AAC CTC ATC GAG TAC CTC TGC AAG AAC TTC GGC ACA GAT	144
Leu Leu Leu Asn Leu Ile Glu Tyr Leu Cys Lys Asn Phe Gly Thr Asp	
195	200
205	
CCC GAA GTG ACT GAC TTG GTC CAG AGC ACG CGG ATC CAC ATC ATG CCG	192
Pro Glu Val Thr Asp Leu Val Gln Ser Thr Arg Ile His Ile Met Pro	
210	215
220	
TCC ATG AAC CCA GAT GGC TAC GAG AAG TCC CAG GAA GGA GAC AGA GGA	240

Ser Met Asn Pro Asp Gly Tyr Glu Lys Ser Gln Glu Gly Asp Arg Gly	
225 230 235 240	
GGC ACC GTT GGC AGA AAT AAC AGC AAC AAC TAC GAC CTG AAC CGG AAC	288
Gly Thr Val Gly Arg Asn Asn Ser Asn Asn Tyr Asp Leu Asn Arg Asn	
245 250 255	
TTC CCA GAT CAG TTC TTC CAG GTG ACA GAC CCT CCG CAG CCA GAA ACT	336
Phe Pro Asp Gln Phe Phe Gln Val Thr Asp Pro Pro Gln Pro Glu Thr	
260 265 270	
CTT GCT GTC ATG AGC TGG TTG AAA ACT TAC CCG TTC GTG CTT TCA GCA	384
Leu Ala Val Met Ser Trp Leu Lys Thr Tyr Pro Phe Val Leu Ser Ala	
275 280 285	
AAC CTG CAT GGA GGT TCT CTG GTG GTT AAT TAC CCT TTT GAT GAC GAT	432
Asn Leu His Gly Gly Ser Leu Val Val Asn Tyr Pro Phe Asp Asp Asp	
290 295 300	
GAA CAA GGA ATA GCC ATA TAC AGT AAA TCC CCA GAC GAT GCT GTG TTT	480
Glu Gln Gly Ile Ala Ile Tyr Ser Lys Ser Pro Asp Asp Ala Val Phe	
305 310 315 320	
CAG CAG CTG GCA CTT TCC TAC TCC AAG GAA AAC AAA AAG ATG TAT CAG	528
Gln Gln Leu Ala Leu Ser Tyr Ser Lys Glu Asn Lys Lys Met Tyr Gln	
325 330 335	
GGA AGC CCT TGT AAG GAT TTG TAC CCC ACA GAG TAC TTT CCA CAT GGC	576
Gly Ser Pro Cys Lys Asp Leu Tyr Pro Thr Glu Tyr Phe Pro His Gly	
340 345 350	
ATC ACG AAC GGG GCC CAG TGG TAC AAC GTT CCA GGT GGG ATG CAG GAC	624
Ile Thr Asn Gly Ala Gln Trp Tyr Asn Val Pro Gly Gly Met Gln Asp	
355 360 365	
TGG AAT TAC TTA AAT ACC AAC CTG TTT GAA GTG ACC ATT GAG CTG GGC	672
Trp Asn Tyr Leu Asn Thr Asn Leu Phe Glu Val Thr Ile Glu Leu Gly	
370 375 380	
TGT GTG AAA TAC CCA AAA GCA GAG GAG CTG CCG AAG TAC TGG GAG CAG	720
Cys Val Lys Tyr Pro Lys Ala Glu Glu Leu Pro Lys Tyr Trp Glu Gln	
385 390 395 400	
AAC CGT AGA TCT CTC CTC CAG TTC ATT AAA CAG GTT CAC CGC GGC ATC	768
Asn Arg Arg Ser Leu Leu Gln Phe Ile Lys Gln Val His Arg Gly Ile	
405 410 415	
TGG GGA TTT GTG CTG GAT GCC ACG GAC GGA AGG GGC ATT CTC AAC GCC	816
Trp Gly Phe Val Leu Asp Ala Thr Asp Gly Arg Gly Ile Leu Asn Ala	
420 425 430	
ACC ATC AGC GTC GCC GAC ATC AAC CAC CCC GTG ACC ACC TAC AAA GAT	864
Thr Ile Ser Val Ala Asp Ile Asn His Pro Val Thr Thr Tyr Lys Asp	
435 440 445	

09018066-080201
102020-99081860

Phe Pro Asp Gln Phe Phe Gln Val Thr Asp Pro Pro Gln Pro Glu Thr
100 105 110

Leu Ala Val Met Ser Trp Leu Lys Thr Tyr Pro Phe Val Leu Ser Ala
115 120 125

Asn Leu His Gly Gly Ser Leu Val Val Asn Tyr Pro Phe Asp Asp Asp
130 135 140

Glu Gln Gly Ile Ala Ile Tyr Ser Lys Ser Pro Asp Asp Ala Val Phe
145 150 155 160

Gln Gln Leu Ala Leu Ser Tyr Ser Lys Glu Asn Lys Lys Met Tyr Gln
165 170 175

Gly Ser Pro Cys Lys Asp Leu Tyr Pro Thr Glu Tyr Phe Pro His Gly
180 185 190

Ile Thr Asn Gly Ala Gln Trp Tyr Asn Val Pro Gly Gly Met Gln Asp
195 200 205

Trp Asn Tyr Leu Asn Thr Asn Leu Phe Glu Val Thr Ile Glu Leu Gly
210 215 220

Cys Val Lys Tyr Pro Lys Ala Glu Glu Leu Pro Lys Tyr Trp Glu Gln
225 230 235 240

Asn Arg Arg Ser Leu Leu Gln Phe Ile Lys Gln Val His Arg Gly Ile
245 250 255

Trp Gly Phe Val Leu Asp Ala Thr Asp Gly Arg Gly Ile Leu Asn Ala
260 265 270

Thr Ile Ser Val Ala Asp Ile Asn His Pro Val Thr Thr Tyr Lys Asp
275 280 285

Gly Asp Tyr Trp Arg Leu Leu Val Gln Gly Thr Tyr Lys Val Thr Ala
290 295 300

Ser Ala Arg Gly Tyr Asp Pro Val Thr Lys Thr Val Glu Val Asp Ser
305 310 315 320

Lys Gly Gly Val Gln Val Asn Phe Thr Leu Ser Arg Thr Asp Ala Lys
325 330 335

Val Glu Glu Gly Lys Val Pro Val Leu Asn Thr Pro Asp Thr Ser Asp
340 345 350

Pro Asn Glu Lys Glu Phe Glu Thr Leu Ile Lys Asp Leu Ser Ala Glu
355 360 365

Asn Gly Leu Glu
370

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TTT GTC CAG GAC AAG AGT GGC AAG GCA ATT TCT AAA GCT ACC ATT GTC	48
Phe Val Gln Asp Lys Ser Gly Lys Ala Ile Ser Lys Ala Thr Ile Val	
375 380 385	
CTT AAT GAA GGC TTG AGG GTC TAC ACT AAA GAA GGT GGC TAT TTC CAT	96
Leu Asn Glu Gly Leu Arg Val Tyr Thr Lys Glu Gly Gly Tyr Phe His	
390 395 400	
GTG CTG TTG GCT CCT GGT TTG CAT AAC ATC AAT GCG ATA GCG GAT GGG	144
Val Leu Leu Ala Pro Gly Leu His Asn Ile Asn Ala Ile Ala Asp Gly	
405 410 415	
TAC CAA CAA AAG CAT ATG AAG GTC TTG GTA CGC CAC GAT GCA CCC AGC	192
Tyr Gln Gln Lys His Met Lys Val Leu Val Arg His Asp Ala Pro Ser	
420 425 430 435	
TCT GTG TTC ATG GTA TTT GAC ATG GAA AAC AGG ATA TTT GGT CTG CCT	240
Ser Val Phe Met Val Phe Asp Met Glu Asn Arg Ile Phe Gly Leu Pro	
440 445 450	
CGA GAG CTG GTT GTA ACT GTT GCA GGT GCA ATT ATG TCT GCT TTG GTC	288
Arg Glu Leu Val Val Thr Val Ala Gly Ala Ile Met Ser Ala Leu Val	
455 460 465	
CTC ACT GCC TGT ATC ATC TGG TGT GTC TGC TCA ATC AAG GCC AAC AGA	336
Leu Thr Ala Cys Ile Ile Trp Cys Val Cys Ser Ile Lys Ala Asn Arg	
470 475 480	
CAC AAA GAT GGC TTC CAC TGC CGG CAG CAC CAC GAC GAT TAC GAG GAC	384
His Lys Asp Gly Phe His Cys Arg Gln His His Asp Asp Tyr Glu Asp	
485 490 495	
GAA ATC CGC ATG ATG TCC ACT GGC TCA AAG AAA TCC CTT TTG AGC CAC	432
Glu Ile Arg Met Met Ser Thr Gly Ser Lys Lys Ser Leu Leu Ser His	
500 505 510 515	
GAA TTC CAG GAT GAA ACA GAC ACT GAA GAA	462
Glu Phe Gln Asp Glu Thr Asp Thr Glu Glu	
520	

09616066 090201

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Phe Val Gln Asp Lys Ser Gly Lys Ala Ile Ser Lys Ala Thr Ile Val
1 5 10 15
Leu Asn Glu Gly Leu Arg Val Tyr Thr Lys Glu Gly Gly Tyr Phe His
20 25 30
Val Leu Leu Ala Pro Gly Leu His Asn Ile Asn Ala Ile Ala Asp Gly
35 40 45
Tyr Gln Gln Lys His Met Lys Val Leu Val Arg His Asp Ala Pro Ser
50 55 60
Ser Val Phe Met Val Phe Asp Met Glu Asn Arg Ile Phe Gly Leu Pro
65 70 75 80
Arg Glu Leu Val Val Thr Val Ala Gly Ala Ile Met Ser Ala Leu Val
85 90 95
Leu Thr Ala Cys Ile Ile Trp Cys Val Cys Ser Ile Lys Ala Asn Arg
100 105 110
His Lys Asp Gly Phe His Cys Arg Gln His His Asp Asp Tyr Glu Asp
115 120 125
Glu Ile Arg Met Met Ser Thr Gly Ser Lys Lys Ser Leu Leu Ser His
130 135 140
Glu Phe Gln Asp Glu Thr Asp Thr Glu
145 150

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

102030-99031360

His Gly Gly Ile Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr
1 5 10 15

Thr Val Ser Thr Ile Pro Pro Pro Ala Ser Thr Asn Arg Trp Ser Gly
20 25 30

Arg Trp Pro Thr Pro Ile Ser Pro Pro Leu Arg Asp Ser His Pro Gln
35 40 45

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro Gln Glu Ile Pro
1 5 10 15

Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala Arg Glu Ala Phe
20 25 30

Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr Thr Ile Pro Pro
35 40 45

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Lys Ala Arg Glu Ala Phe Arg Arg
1 5

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asp Val Ser Gly Val Leu Phe Gln Tyr Pro Asp Thr Glu Gly Lys
1 5 10 15

102030-33031360

00010000 00000000

GAG GCG GCG CGG TGC ATC GAG CAG CTG CTG CCG CGG CAC GAT GAC TTC	48
Glu Ala Ala Arg Cys Ile Glu Gln Leu Leu Pro Arg His Asp Asp Phe	
1 5 10 15	
TCC CGG CGG CAC ATC GGC CCC CGG GAG GGG GAG AAG AGG GAG ATG CTG	96
Ser Arg Arg His Ile Gly Pro Arg Glu Gly Glu Lys Arg Glu Met Leu	
20 25 30	
CGA GCC CTC GGG GTG CAG AGC GTC GAG GAG CTG ATG GAT AAA GCC ATC	144
Arg Ala Leu Gly Val Gln Ser Val Glu Glu Leu Met Asp Lys Ala Ile	
35 40 45	
CCG GGC AGC ATC CGG CTG CGC AGG CCG CTG AGG ATG GAG GAC CCC GTG	192
Pro Gly Ser Ile Arg Leu Arg Arg Pro Leu Arg Met Glu Asp Pro Val	
50 55 60	
GGT GAA AAT GAA ATC CTT GAA ACT TTA TAC AAT ATT GCA AGC AAG AAC	240
Gly Glu Asn Glu Ile Leu Glu Thr Leu Tyr Asn Ile Ala Ser Lys Asn	
65 70 75 80	
AAG ATA TGG AGG TCC TAT ATA GGC ATG GGT TAT TAC AAC TGC TCA GTG	288
Lys Ile Trp Arg Ser Tyr Ile Gly Met Gly Tyr Tyr Asn Cys Ser Val	
85 90 95	
CCT CAA CCC ATT GCA CGG AAT TTG TTG GAG AAT GCA GGA TGG GTT ACC	336
Pro Gln Pro Ile Ala Arg Asn Leu Leu Glu Asn Ala Gly Trp Val Thr	
100 105 110	
CAG TAT ACT CCC TAC CAA CCT GAG GTC TCA CAG GGC AGG CTG GAG AGC	384
Gln Tyr Thr Pro Tyr Gln Pro Glu Val Ser Gln Gly Arg Leu Glu Ser	
115 120 125	
CTG CTA AAT TAC CAG ACT ATG GTG TGT GAT ATC ACA GGA ATG GAT GTG	432
Leu Leu Asn Tyr Gln Thr Met Val Cys Asp Ile Thr Gly Met Asp Val	
130 135 140	
GCT AAT GCA TCA TTG CTG GAT GAG GGG ACA GCT GCT GCA GAA GCT ATG	480
Ala Asn Ala Ser Leu Leu Asp Glu Gly Thr Ala Ala Ala Glu Ala Met	
145 150 155 160	
CAA TTA TGT CAC AGG CAC AAC AAA AGG AGG AAG TTT TAT GTA GAT TCC	528
Gln Leu Cys His Arg His Asn Lys Arg Arg Lys Phe Tyr Val Asp Ser	
165 170 175	
CGA TGC CAC CCT CAG ACT ATA GCA GTG GTC CAA ACT AGA GCC AAT TAT	576
Arg Cys His Pro Gln Thr Ile Ala Val Val Gln Thr Arg Ala Asn Tyr	
180 185 190	
ACA GGT GTT ATT ACT GAG CTC AAA TTA CCC CAT GAG ATG GAT TTC AGT	624
Thr Gly Val Ile Thr Glu Leu Lys Leu Pro His Glu Met Asp Phe Ser	
195 200 205	
GGA AAG GAT GTC AGT GGA GTA TTA TTT CAG TAT CCA GAC ACT GAG GGG	672
Gly Lys Asp Val Ser Gly Val Leu Phe Gln Tyr Pro Asp Thr Glu Gly	

210	215	220	
AAG GTG GAA GAC TTC TCT GAA CTT GTT GAA AGA GCT CAT CAG AAC GGG			720
Lys Val Glu Asp Phe Ser Glu Leu Val Glu Arg Ala His Gln Asn Gly			
225	230	235	240
ACT CTT GCC TGC TGT GCT ACT GAT CTT CTG GCT CTC TGT ATT CTG AAG			768
Thr Leu Ala Cys Cys Ala Thr Asp Leu Leu Ala Leu Cys Ile Leu Lys			
	245	250	255
CCT CCT GGA GAG TTT GGG GTA GAT GTT GTC CTG GGT AGC TCC CAG AGA			816
Pro Pro Gly Glu Phe Gly Val Asp Val Val Leu Gly Ser Ser Gln Arg			
	260	265	270
TTT GGT GTG CCA CTC TGC TAT GGG GGA CCC CAC GCA GCA TTC TTC GCT			864
Phe Gly Val Pro Leu Cys Tyr Gly Gly Pro His Ala Ala Phe Phe Ala			
	275	280	285
GTC AAG GAA AAC CTA GTG AGA ATG ATG CCA GGC AGG ATG GTG GGT GTC			912
Val Lys Glu Asn Leu Val Arg Met Met Pro Gly Arg Met Val Gly Val			
	290	295	300
ACA AGA GAT GCA AAT GGA AAA GAA GTT TAC CGA CTG GCT TTA CAA ACA			960
Thr Arg Asp Ala Asn Gly Lys Glu Val Tyr Arg Leu Ala Leu Gln Thr			
305	310	315	320
CGA GAG CAG CAT ATC AGG AGG GAC AAA GCT ACA AGC AAC ATC TGC ACA			1008
Arg Glu Gln His Ile Arg Arg Asp Lys Ala Thr Ser Asn Ile Cys Thr			
	325	330	335
GCA CAG GCT CTT CTG GCT AAT ATG GCA GCC ATG TTT GGT GTC TAC CAT			1056
Ala Gln Ala Leu Leu Ala Asn Met Ala Ala Met Phe Gly Val Tyr His			
	340	345	350
GGG TCT GAT GGA TTA AGG GAT ATT GCA AGA CGG GTA CAC AAT GCT ACT			1104
Gly Ser Asp Gly Leu Arg Asp Ile Ala Arg Arg Val His Asn Ala Thr			
	355	360	365
TTA ATC CTG GCT GAA GGT CTC AGG AGA GCT GGT CAT AAA CTG CAC CAT			1152
Leu Ile Leu Ala Glu Gly Leu Arg Arg Ala Gly His Lys Leu His His			
	370	375	380
GAT CTG TTC TTT GAT ACC TTG ACA GTC ACG TGT GGA TGC TCA GTC AAA			1200
Asp Leu Phe Phe Asp Thr Leu Thr Val Thr Cys Gly Cys Ser Val Lys			
385	390	395	400
GAA GTT TTG GAC AGG GCA GCT CTT AGA AAG ATA AAT TTT CGC ATT TAT			1248
Glu Val Leu Asp Arg Ala Ala Leu Arg Lys Ile Asn Phe Arg Ile Tyr			
	405	410	415
AGT GAT GGC AGA CTT GGA GTA TCA CTT GAT GAA ACT GTA AGT GAG AAA			1296
Ser Asp Gly Arg Leu Gly Val Ser Leu Asp Glu Thr Val Ser Glu Lys			
	420	425	430

GAC Asp	CTA Leu	GAT Asp	GAC Asp	ATA Ile	TTA Leu	TGG Trp	ATT Ile	TTT Phe	GGT Gly	TGC Cys	GAG Glu	TCT Ser	TCA Ser	GCT Ala	GAA Glu	1344
435440445																
CTA Leu	ATT Ile	GCT Ala	GAA Glu	GGT Gly	ATG Met	GGC Gly	GAG Glu	GAA Glu	ACC Thr	AAA Lys	GGT Gly	ATC Ile	CTT Leu	AGC Ser	ACC Thr	1392
450455460																
CCA Pro	TTT Phe	AAG Lys	AGA Arg	ACT Thr	TCC Ser	AAA Lys	TTC Phe	TTG Leu	ACC Thr	CAT His	CAG Gln	GTT Val	TTC Phe	AAC Asn	AGC Ser	1440
465470475480																
TAT Tyr	CAC His	TCC Ser	GAA Glu	ACA Thr	AAT Asn	ATC Ile	GTA Val	CGG Arg	TAC Tyr	ATG Met	AAG Lys	AGA Arg	TTA Leu	GAA Glu	AAC Asn	1488
485490495																
AAA Lys	GAT Asp	ATT Ile	TCC Ser	CTT Leu	GTT Val	CAC His	AGC Ser	ATG Met	ATT Ile	CCT Pro	TTG Leu	GGG Gly	TCC Ser	TGT Cys	ACA Thr	1536
500505510																
ATG Met	AAG Lys	CTC Leu	AAT Asn	AGT Ser	TCA Ser	GCT Ala	GAA Glu	CTT Leu	GCA Ala	CCT Pro	ATT Ile	TCA Ser	TGG Trp	AAG Lys	GAA Glu	1584
515520525																
TTT Phe	GCC Ala	AAC Asn	ATC Ile	CAC His	CCC Pro	TTT Phe	GTG Val	CCC Pro	TTG Leu	GAT Asp	CAA Gln	GCT Ala	CAA Gln	GGG Gly	TAT Tyr	1632
530535540																
CAG Gln	CAG Gln	CTT Leu	TTC Phe	AAG Lys	GAC Asp	TTA Leu	GAG Glu	AAG Lys	GAC Asp	CTG Leu	TGT Cys	GAG Glu	ATT Ile	ACT Thr	GGT Gly	1680
545550555560																
TAC Tyr	GAC Asp	AAA Lys	ATC Ile	TCC Ser	TTC Phe	CAA Gln	CCA Pro	AAC Asn	AGT Ser	GGA Gly	GCC Ala	CAA Gln	GGA Gly	GAG Glu	TAC Tyr	1728
565570575																
GCA Ala	GGC Gly	TTG Leu	GCC Ala	GCA Ala	ATC Ile	AAA Lys	GCT Ala	TAT Tyr	TTA Leu	AAT Asn	GCA Ala	AAA Lys	GGA Gly	GAA Glu	CGT Arg	1776
580585590																
CAT His	CGA Arg	AGT Ser	GTT Val	TGC Cys	CTT Leu	ATT Ile	CCT Pro	AGA Arg	TCT Ser	GCT Ala	CAT His	GGT Gly	ACA Thr	AAT Asn	CCA Pro	1824
595600605																
GCA Ala	AGT Ser	GCA Ala	CAG Gln	ATG Met	GCA Ala	GGG Gly	ATG Met	AAG Lys	ATT Ile	CAA Gln	CCA Pro	GTT Val	GAA Glu	GTA Val	GAT Asp	1872
610615620																
AAA Lys	AAT Asn	GGG Gly	AGC Ser	ATT Ile	GAT Asp	ATC Ile	TCC Ser	CAT His	TTA Leu	AAA Lys	GCA Ala	ATG Met	GTG Val	GAC Asp	AAA Lys	1920
625630635640																
CAC His	AAG Lys	GAG Glu	AAC Asn	CTG Leu	GCA Ala	GCC Ala	ATC Ile	ATG Met	ATC Ile	ACA Thr	TAC Tyr	CCT Pro	TCC Ser	ACC Thr	AAT Asn	1968

645	650	655	
GGT GTG TTT GAG GAG GAG ATT GGG GAT GTG TGT GAG CTG ATT CAC AAA Gly Val Phe Glu Glu Glu Ile Gly Asp Val Cys Glu Leu Ile His Lys 660 665 670			2016
AAC GGA GGC CAG GTT TAC CTG GAT GGA GCA AAC ATG AAC GCC CAA GTG Asn Gly Gly Gln Val Tyr Leu Asp Gly Ala Asn Met Asn Ala Gln Val 675 680 685			2064
GGT CTG TGT CGT CCT GGA GAT TAT GGC TCT GAT GTC TCT CAC TTA AAC Gly Leu Cys Arg Pro Gly Asp Tyr Gly Ser Asp Val Ser His Leu Asn 690 695 700			2112
CTT CAC AAA ACC TTT TGC ATT CCC CAT GGA GGA GGA GGA CCT GGA ATG Leu His Lys Thr Phe Cys Ile Pro His Gly Gly Gly Gly Pro Gly Met 705 710 715 720			2160
GGA CCA ATT GGA GTG AAG AAA CAT CTG GCT CCC TAC TTG CCT ACC CAT Gly Pro Ile Gly Val Lys Lys His Leu Ala Pro Tyr Leu Pro Thr His 725 730 735			2208
CCT GTC ATC AAG ATT CAG ACG GAT AAG GAT GCA TGT CCT TTG GGT ACT Pro Val Ile Lys Ile Gln Thr Asp Lys Asp Ala Cys Pro Leu Gly Thr 740 745 750			2256
GTC AGT GCT GCA CCT TGG GGT TCC AGT GCT ATA TTG CCT ATT TCC TGG Val Ser Ala Ala Pro Trp Gly Ser Ser Ala Ile Leu Pro Ile Ser Trp 755 760 765			2304
GTG TAT ATC AAG ACA ATG GGA GCA AAG GGT CTT AAA CAC GCT TCT GAG Val Tyr Ile Lys Thr Met Gly Ala Lys Gly Leu Lys His Ala Ser Glu 770 775 780			2352
GTT GCT ATA TTA AAT GCA AAC TAC ATG GCA AAG AGG CTG GAG AAG CAC Val Ala Ile Leu Asn Ala Asn Tyr Met Ala Lys Arg Leu Glu Lys His 785 790 795 800			2400
TAC AAA ATC CTT TTC AGA GGA GTA AGA GGT TAT GTA GCC CAT GAA TTC Tyr Lys Ile Leu Phe Arg Gly Val Arg Gly Tyr Val Ala His Glu Phe 805 810 815			2448
ATT TTG GAT ACA AGA CCT TTC AAA AAA ACA GCA AAC ATT GAA GCT GTG Ile Leu Asp Thr Arg Pro Phe Lys Lys Thr Ala Asn Ile Glu Ala Val 820 825 830			2496
GAT CTT GCT AAG CGA CTT CAG GAT TAT GGT TTT CAT GCT CCA ACC ATG Asp Leu Ala Lys Arg Leu Gln Asp Tyr Gly Phe His Ala Pro Thr Met 835 840 845			2544
TCC TGG CCA GTG GCA GGC ACA CTT ATG ATT GAA CCA ACA GAG TCT GAA Ser Trp Pro Val Ala Gly Thr Leu Met Ile Glu Pro Thr Glu Ser Glu 850 855 860			2592

09613066 030201

GAC AAG GCA GAG CTG GAC AGG TTT TGT GAT GCA ATG ATC AGT ATT CGA 2640
 Asp Lys Ala Glu Leu Asp Arg Phe Cys Asp Ala Met Ile Ser Ile Arg
 865 870 875 880

CAG GAA ATT GCT GAA ATA GAG GAG GGC AGG ATG GAC CCT CAG ATT AAC 2688
 Gln Glu Ile Ala Glu Ile Glu Glu Gly Arg Met Asp Pro Gln Ile Asn
 885 890 895

CCA TTA AAG ATG TCA CCA CAT ACT CTA AAC TGT GTC ACT TCT TCA AAG 2736
 Pro Leu Lys Met Ser Pro His Thr Leu Asn Cys Val Thr Ser Ser Lys
 900 905 910

TGG GAT CGT CCT TAT TCC AGA GAA GTG GCA GCA TTC CCA CTG CCG TTT 2784
 Trp Asp Arg Pro Tyr Ser Arg Glu Val Ala Ala Phe Pro Leu Pro Phe
 915 920 925

GTG AAA CCT GAG AGC AAG TTT TGG CCC ACA ATT GCT CGC ATC GAT GAC 2832
 Val Lys Pro Glu Ser Lys Phe Trp Pro Thr Ile Ala Arg Ile Asp Asp
 930 935 940

ATA TAC GGA GAT CAA CAC CTG GTT TGT ACC TGC CCA CCG ATG GAA GCC 2880
 Ile Tyr Gly Asp Gln His Leu Val Cys Thr Cys Pro Pro Met Glu Ala
 945 950 955 960

TAC GAA TCT CCC TTC TCT GAA CAG AAG AGA GCA TCT TCG TAA 2922
 Tyr Glu Ser Pro Phe Ser Glu Gln Lys Arg Ala Ser Ser
 965 970

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 973 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Glu Ala Ala Arg Cys Ile Glu Gln Leu Leu Pro Arg His Asp Asp Phe
 1 5 10 15
 Ser Arg Arg His Ile Gly Pro Arg Glu Gly Glu Lys Arg Glu Met Leu
 20 25 30
 Arg Ala Leu Gly Val Gln Ser Val Glu Glu Leu Met Asp Lys Ala Ile
 35 40 45
 Pro Gly Ser Ile Arg Leu Arg Arg Pro Leu Arg Met Glu Asp Pro Val
 50 55 60
 Gly Glu Asn Glu Ile Leu Glu Thr Leu Tyr Asn Ile Ala Ser Lys Asn
 65 70 75 80

102030-93081260

Lys	Ile	Trp	Arg	Ser	Tyr	Ile	Gly	Met	Gly	Tyr	Tyr	Asn	Cys	Ser	Val	85	90	95	
Pro	Gln	Pro	Ile	Ala	Arg	Asn	Leu	Leu	Glu	Asn	Ala	Gly	Trp	Val	Thr	100	105	110	
Gln	Tyr	Thr	Pro	Tyr	Gln	Pro	Glu	Val	Ser	Gln	Gly	Arg	Leu	Glu	Ser	115	120	125	
Leu	Leu	Asn	Tyr	Gln	Thr	Met	Val	Cys	Asp	Ile	Thr	Gly	Met	Asp	Val	130	135	140	
Ala	Asn	Ala	Ser	Leu	Leu	Asp	Glu	Gly	Thr	Ala	Ala	Ala	Glu	Ala	Met	145	150	155	160
Gln	Leu	Cys	His	Arg	His	Asn	Lys	Arg	Arg	Lys	Phe	Tyr	Val	Asp	Ser	165	170	175	
Arg	Cys	His	Pro	Gln	Thr	Ile	Ala	Val	Val	Gln	Thr	Arg	Ala	Asn	Tyr	180	185	190	
Thr	Gly	Val	Ile	Thr	Glu	Leu	Lys	Leu	Pro	His	Glu	Met	Asp	Phe	Ser	195	200	205	
Gly	Lys	Asp	Val	Ser	Gly	Val	Leu	Phe	Gln	Tyr	Pro	Asp	Thr	Glu	Gly	210	215	220	
Lys	Val	Glu	Asp	Phe	Ser	Glu	Leu	Val	Glu	Arg	Ala	His	Gln	Asn	Gly	225	230	235	240
Thr	Leu	Ala	Cys	Cys	Ala	Thr	Asp	Leu	Leu	Ala	Leu	Cys	Ile	Leu	Lys	245	250	255	
Pro	Pro	Gly	Glu	Phe	Gly	Val	Asp	Val	Val	Leu	Gly	Ser	Ser	Gln	Arg	260	265	270	
Phe	Gly	Val	Pro	Leu	Cys	Tyr	Gly	Gly	Pro	His	Ala	Ala	Phe	Phe	Ala	275	280	285	
Val	Lys	Glu	Asn	Leu	Val	Arg	Met	Met	Pro	Gly	Arg	Met	Val	Gly	Val	290	295	300	
Thr	Arg	Asp	Ala	Asn	Gly	Lys	Glu	Val	Tyr	Arg	Leu	Ala	Leu	Gln	Thr	305	310	315	320
Arg	Glu	Gln	His	Ile	Arg	Arg	Asp	Lys	Ala	Thr	Ser	Asn	Ile	Cys	Thr	325	330	335	
Ala	Gln	Ala	Leu	Leu	Ala	Asn	Met	Ala	Ala	Met	Phe	Gly	Val	Tyr	His	340	345	350	
Gly	Ser	Asp	Gly	Leu	Arg	Asp	Ile	Ala	Arg	Arg	Val	His	Asn	Ala	Thr	355	360	365	

102030-99021360

Leu	Ile	Leu	Ala	Glu	Gly	Leu	Arg	Arg	Ala	Gly	His	Lys	Leu	His	His
370						375					380				
Asp	Leu	Phe	Phe	Asp	Thr	Leu	Thr	Val	Thr	Cys	Gly	Cys	Ser	Val	Lys
385					390					395					400
Glu	Val	Leu	Asp	Arg	Ala	Ala	Leu	Arg	Lys	Ile	Asn	Phe	Arg	Ile	Tyr
			405						410					415	
Ser	Asp	Gly	Arg	Leu	Gly	Val	Ser	Leu	Asp	Glu	Thr	Val	Ser	Glu	Lys
			420					425					430		
Asp	Leu	Asp	Asp	Ile	Leu	Trp	Ile	Phe	Gly	Cys	Glu	Ser	Ser	Ala	Glu
	435						440					445			
Leu	Ile	Ala	Glu	Gly	Met	Gly	Glu	Glu	Thr	Lys	Gly	Ile	Leu	Ser	Thr
450						455					460				
Pro	Phe	Lys	Arg	Thr	Ser	Lys	Phe	Leu	Thr	His	Gln	Val	Phe	Asn	Ser
465					470					475					480
Tyr	His	Ser	Glu	Thr	Asn	Ile	Val	Arg	Tyr	Met	Lys	Arg	Leu	Glu	Asn
			485						490					495	
Lys	Asp	Ile	Ser	Leu	Val	His	Ser	Met	Ile	Pro	Leu	Gly	Ser	Cys	Thr
			500					505					510		
Met	Lys	Leu	Asn	Ser	Ser	Ala	Glu	Leu	Ala	Pro	Ile	Ser	Trp	Lys	Glu
		515					520					525			
Phe	Ala	Asn	Ile	His	Pro	Phe	Val	Pro	Leu	Asp	Gln	Ala	Gln	Gly	Tyr
	530					535					540				
Gln	Gln	Leu	Phe	Lys	Asp	Leu	Glu	Lys	Asp	Leu	Cys	Glu	Ile	Thr	Gly
545				550					555						560
Tyr	Asp	Lys	Ile	Ser	Phe	Gln	Pro	Asn	Ser	Gly	Ala	Gln	Gly	Glu	Tyr
			565					570					575		
Ala	Gly	Leu	Ala	Ala	Ile	Lys	Ala	Tyr	Leu	Asn	Ala	Lys	Gly	Glu	Arg
		580						585					590		
His	Arg	Ser	Val	Cys	Leu	Ile	Pro	Arg	Ser	Ala	His	Gly	Thr	Asn	Pro
		595					600					605			
Ala	Ser	Ala	Gln	Met	Ala	Gly	Met	Lys	Ile	Gln	Pro	Val	Glu	Val	Asp
	610					615					620				
Lys	Asn	Gly	Ser	Ile	Asp	Ile	Ser	His	Leu	Lys	Ala	Met	Val	Asp	Lys
625				630					635					640	
His	Lys	Glu	Asn	Leu	Ala	Ala	Ile	Met	Ile	Thr	Tyr	Pro	Ser	Thr	Asn
			645					650						655	

102030-99031260

Gly	Val	Phe	Glu	Glu	Glu	Ile	Gly	Asp	Val	Cys	Glu	Leu	Ile	His	Lys	
			660					665					670			
Asn	Gly	Gly	Gln	Val	Tyr	Leu	Asp	Gly	Ala	Asn	Met	Asn	Ala	Gln	Val	
		675					680					685				
Gly	Leu	Cys	Arg	Pro	Gly	Asp	Tyr	Gly	Ser	Asp	Val	Ser	His	Leu	Asn	
		690				695					700					
Leu	His	Lys	Thr	Phe	Cys	Ile	Pro	His	Gly	Gly	Gly	Gly	Pro	Gly	Met	
	705				710					715					720	
Gly	Pro	Ile	Gly	Val	Lys	Lys	His	Leu	Ala	Pro	Tyr	Leu	Pro	Thr	His	
				725					730						735	
Pro	Val	Ile	Lys	Ile	Gln	Thr	Asp	Lys	Asp	Ala	Cys	Pro	Leu	Gly	Thr	
			740					745					750			
Val	Ser	Ala	Ala	Pro	Trp	Gly	Ser	Ser	Ala	Ile	Leu	Pro	Ile	Ser	Trp	
		755					760					765				
Val	Tyr	Ile	Lys	Thr	Met	Gly	Ala	Lys	Gly	Leu	Lys	His	Ala	Ser	Glu	
	770					775					780					
Val	Ala	Ile	Leu	Asn	Ala	Asn	Tyr	Met	Ala	Lys	Arg	Leu	Glu	Lys	His	
	785				790					795					800	
Tyr	Lys	Ile	Leu	Phe	Arg	Gly	Val	Arg	Gly	Tyr	Val	Ala	His	Glu	Phe	
				805					810					815		
Ile	Leu	Asp	Thr	Arg	Pro	Phe	Lys	Lys	Thr	Ala	Asn	Ile	Glu	Ala	Val	
			820					825					830			
Asp	Leu	Ala	Lys	Arg	Leu	Gln	Asp	Tyr	Gly	Phe	His	Ala	Pro	Thr	Met	
		835					840					845				
Ser	Trp	Pro	Val	Ala	Gly	Thr	Leu	Met	Ile	Glu	Pro	Thr	Glu	Ser	Glu	
	850					855					860					
Asp	Lys	Ala	Glu	Leu	Asp	Arg	Phe	Cys	Asp	Ala	Met	Ile	Ser	Ile	Arg	
	865				870					875					880	
Gln	Glu	Ile	Ala	Glu	Ile	Glu	Glu	Gly	Arg	Met	Asp	Pro	Gln	Ile	Asn	
				885				890					895			
Pro	Leu	Lys	Met	Ser	Pro	His	Thr	Leu	Asn	Cys	Val	Thr	Ser	Ser	Lys	
			900					905					910			
Trp	Asp	Arg	Pro	Tyr	Ser	Arg	Glu	Val	Ala	Ala	Phe	Pro	Leu	Pro	Phe	
		915					920					925				
Val	Lys	Pro	Glu	Ser	Lys	Phe	Trp	Pro	Thr	Ile	Ala	Arg	Ile	Asp	Asp	

930

935

940

Ile Tyr Gly Asp Gln His Leu Val Cys Thr Cys Pro Pro Met Glu Ala
945 950 955 960

Tyr Glu Ser Pro Phe Ser Glu Gln Lys Arg Ala Ser Ser
965 970

FOI2080-39081850